REMARKS

I. Status of the Claims

Claims 1-14, 17, 67, 68, and 70-72 are pending. Claims 1-14, 17, 67, 68, and 70-72 are rejected. In the amendments presented above, claim 1 has been amended to correct a typographical error. Claims 6 and 7 have been amended to remove the term "about" for agreement with claims 2 and 1, respectively. Claims 70 and 71 have been canceled herein. After entry of the amendments above, claims 1-14, 17, 67, 68 and 72 will remain pending.

Applicants respectfully request reconsideration of claims 1-14, 17, 67, 68, and 72.

II. Claims 1-6, 12-14, 17, 67, 68 and 72 are Patentable over Kallioniemi, McGill, Pollack, in view of GibcoBRL Catalog, and Mackey

Applicants traverse the rejection of claims 1-6, 12-14, 17, 67, 68 and 72 under § 103(a) over Kallioniemi (U.S. 2002/0132246 A1), McGill (US 5,658,730), Pollack (Nature Genetics, vol. 23, pp. 41-46, September 1999), in view of GibcoBRL Catalog (pages 18-15 and 18-16, 1995-96) and Mackey (Anal. Biochem., vol. 212, pp. 428-435, 1993).

It is improper to interpret the term "about" as any number of bases. It is well accepted that terms such as "about" are interpreted with reference what the person of ordinary skill in the art would understand in light of the specification. Under no situation, however, would the term "about" be interpreted to include any number of bases as erroneously proffered.

Kallioniemi, either alone or in combination with any secondary citation, does not render claim 1 obvious. In particular, Kallioniemi fails to disclose, teach or suggest a method that uses, in part, a plurality of immobilized nucleic acid probes that are a collection of clones that represent all of a chromosome or a genome of an organism, and contacting such probes with labeled, double-stranded genomic DNA fragments. Instead, Kallioniemi describes a genosensor that scans the human genome for large deletions or duplications in a single assay (emphasis added, page 14 Par. No. [0152], [0153]). Scanning the human genome using a genosensor is not the same as a method that uses a

plurality of immobilized nucleic acid probes that are a collection of clones that represent all of a chromosome or a genome of an organism as defined by claim 1.

In addition, Kallioniemi does not disclose, teach, or suggest a method that uses an array of clones at known locations. The Office Action asserts that FIG. 14 of Kallioniemi teaches an array of clones at known locations. At Par. No. [0048] of Kallioniemi, it states "FIG. 14 is a digital representation of the results of a chromosomal CGH analysis showing high level amplifications in Sum-52 breast cancer cells at 10q25-q26 and at 7q21-q22, a genosensor CGH analysis indicating high level amplifications of the MET (7q21) and FGFR2 (10q25) oncogenes, and a FISH analysis showing amplification of FGFR2 (at 10q25)." Example 10 of Kallioniemi also refers to FIG. 14. No objective evidence has been provided, however, that indicates FIG. 14 of Kallioniemi discloses, teaches or suggests a method that uses an array of clones at known locations.

Kallioniemi also does not disclose, teach or suggest the observing step of claim 1. In particular, Kallioniemi does not disclose, teach or suggest an amount and location of labeled genomic nucleic acid hybridized to each immobilized probe, to detect regions of amplification or deletion in the sample, wherein positional information of clones on the arrays and chromosomes is correlated, thereby generating a molecular profile of the chromosome or genome of the sample genomic nucleic acid. Specifically, Kallioniemi does not disclose, teach or suggest generating a molecular profile of the chromosome or genome of the sample. Instead, Kallioniemi teaches revealing "the relative concentration of each target specific sequence in the probe mixture." (See Kallioniemi at page 15 Par. No. [0157]). Revealing a relative concentration of a target specific sequence is not the same as generating a molecular profile.

As the Examiner acknowledges, Kallioniemi also does not disclose teach or suggest DNA fragments with length of less than about 200 bp to less than about 30 bp. In contrast, Applicants' specification recites that "the compositions and methods of the invention provide fragmented DNA probes to a size range of less than about 200 bases." See Application at Par. No. [0033]. Further, "the superior effectiveness of the methods of the invention may be because DNA probes fragmented to a smaller size (i.e., less than about 200 residues) have a lower possibility of partially hybridizing to closely related sequences..." See Application at Par. No. [0033].

The many deficiencies noted above for Kallioniemi are not cured by any of the secondary citations. With reference to claim 1, McGill does not disclose, teach or suggest the particular size of the labeled, genomic nucleic acid fragments recited in claim 1. It is improper to use the probe size disclosed in McGill to render obvious a method that recites the use of a particular size of the labeled, genomic nucleic acid fragments. As recited in claim 1, these labeled, genomic nucleic acid fragments are contacted with probes.

In addition, no evidence has been provided that the person of ordinary skill in the art would be motivated to combine Kallioniemi with the prostate cancer diagnosis methods of McGill.

Neither the Abstract of Pollack nor page 46, first paragraph of Pollack discloses, teaches or suggest the particular labeled fragment size recited in claim 1, i.e., less than about 200 bases. Thus, even if Pollack does disclose that reducing the size of genomic DNA before labeling improved labeling efficiency, without recitation of a particular size, this disclosure would not be sufficient to render claim 1 obvious.

With reference to the GibcoBRL BioPrime labeling kit, no objective evidence has been provided that this kit discloses, teaches or suggests double-stranded genomic DNA fragments that would necessarily be labeled on both strands.

With reference to the assertion that Mackey provides the motivation to combine Kallioniemi, McGill and Pollack, this assertion is improper. It is well accepted that the motivation to combine citations must exist in the citations themselves. Without some motivation or suggestion in the citations themselves, the citations may not be combined. See MPEP 2143.01.

In view of the above, claims 1-14, 17, 67, 68 and 72 are patentable over Kallioniemi, McGill, Pollack, in view of GibcoBRL Catalog and Mackey.

III. Claims 7, 8, and 10 are Patentable over Kallioniemi, McGill, and Pollack, in view of GibcoBRL Catalog, and Mackey, as applied to claim 1 above, and further in view of Anderson

Applicants traverse the rejection of claims 7, 8, and 10 under § 103(a) over Kallioniemi, McGill, Pollack, in view of GibcoBRL Catalog, and Mackey, as applied to

claim 1 above, and further in view of Anderson (Nucl. Acids Res., vol. 9, pp. 3015-3027, 1981).

Claims 7, 8 and 10 each depends directly or indirectly from claim 1. As discussed above, Kallioniemi, either alone or in combination with any secondary citation, does not render claim 1 obvious. For at least the same reasons, Kallioniemi, either alone or in combination with any secondary citation, does not render claims 7, 8 or 10 obvious. In addition, it is improper to use Anderson as the motivation to combine Kallioniemi, McGill, Pollack and Mackey. As discussed above, the motivation to combine citations must exist in the citations themselves.

Notwithstanding the above, Anderson does not cure the deficiencies of Kallioniemi, McGill, Pollack, GibcoBRL or Mackey. In particular, Anderson does not disclose fragmentation of target, genomic DNA that has both strands labeled with a detectable moiety. Instead, the agarose gel shown in FIG. 1 was obtained by digesting lambda DNA with DNase I. There is no disclosure that both strands of the lambda DNA have been labeled.

Accordingly, the rejection is improper and should be withdrawn.

IV. Claim 9 is Patentable over Kallioniemi, McGill, Pollack, in view of GibcoBRL Catalog and Mackey, in view of Anderson, as applied to claim 8 above, and further in view of Waggoner

Applicants traverse the rejection of claim 9 under § 103(a) over Kallioniemi, McGill, Pollack, in view of GibcoBRL Catalog and Mackey, in view of Anderson, as applied to claim 8 above, and further in view of Waggoner (U.S. 5,268,486).

Claim 9 depends indirectly from claim 1. As discussed above, Kallioniemi, either alone or in combination with any secondary citation, does not render claim 1 obvious. For at least the same reasons, Kallioniemi, either alone or in combination with any secondary citation, does not render claim 9 obvious.

Aside from the above, Waggoner does not cure the deficiencies of Kallioniemi, McGill, Pollack, GibcoBRL or Mackey. Waggoner does not disclose labeling of both strands of genomic DNA and fragmentation or enzymatic digestion of the genomic DNA. Therefore, Waggoner's disclosure of Cy3 and Cy5 does not render claim 9 obvious.

V. Claim 11 is Patentable over Kallioniemi, McGill, Pollack, in view of GibcoBRL Catalog and Mackey, in view of Anderson, as applied to claim 1 above, and further in view of Ordahl and Anderson

Applicants traverse the rejection of claim 11 under § 103(a) over Kallioniemi, McGill, Pollack, in view of GibcoBRL Catalog and Mackey, in view of Anderson, as applied to claim 1 above, and further in view of Ordahl (Nucl. Acids Res., vol. 3, pp. 2985-2999, 1976) and Anderson.

Claim 11 depends indirectly from claim 1. As discussed above, Kallioniemi, either alone or in combination with any secondary citation, does not render claim 1 obvious. For at least the same reasons, Kallioniemi, either alone or in combination with any secondary citation, does not render claim 11 obvious.

Notwithstanding the above, Ordahl discloses a technique that produces DNA fragments of approximately 230 base pairs, whereas claim 11 recites fragmenting to produce sizes smaller than about 200 bases by shearing followed by enzymatic digestion of the sheared DNA with DNase. As discussed above in Section III, Anderson's disclosure of digesting lambda DNA with DNase I is insufficient, because there is no disclosure, teaching or suggestion that both strands of the lambda DNA have been labeled.

In view of the above, claim 11 is patentable over the citations.

VI. Conclusion

In view of the foregoing Amendments and Remarks, this application is in condition for allowance. A notice to this effect is respectfully requested. If the Examiner believes that the application is not in condition for allowance, the Examiner is invited to call Applicants' attorney at the telephone number listed below.

Respectfully submitted,
Allan Bradley et al., Applicants

By: _____

Ann Lamport Hammitte, Reg. No. 34,858
Christopher R. Rhodes, Reg. No. 47,022
LOWRIE, LANDO & ANASTASI, LLP
Riverfront Office Park
One Main Street
Cambridge, MA 02142
Telephone: 617-395-7000
Facsimile: 617-395-7070

Date: November 9, 2006

793694